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HSU131B10 37650 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs
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X; XK membrane transport protein.
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Dodsworth, S.
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AUTHORS
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

TITLE Direct Submiss JOURNAL Submitted (17-		repeat_region	: fragmen
	E-mail enquires: humquery@sanger.ac.uk Clone nerequest@sanger.ac.uk	repeat region	/note="Alu repeat: matches 1 1930019436
COMMENT IMPORTANT: Th	IMPORTANT: This sequence is the entire insert of clone U131B10. The true left end of clone U131B10 is at 1 in this sequence. The) 	/partial /note="Alu repeat: matches 1
true right end Ul31B10 is fro	d of clone U131B10 is at 37650. om the human chromosome X-specific cosmid library.	repeat_region	1944019644 /parrial
FEATURES Locat	tion/Qualifiers	tearer tearer	/note="Alu repeat: matches 1
/orga	anism="Homo sapiens"		
/db_x /chro	<pre>Kref="taxon:9606" DMOSGME="X"</pre>	repeat_region	/note="Alu repeat: matches 242. 1971119870
/map="X" /clone=".	="X" ne="LL0XNC01-131B10"		/partial /note="Alu repeat: matches 149.
/clon	/clone_lib="LLOXNC01" 364	repeat_region	2188122027 /note-"MID element fracment"
	note="MIR element fragment"	repeat_region	Z3139, .23303
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/note repeat region 3347	/note="Alu repeat: matches 3081 of consensus"	repeat_region	2334323508 /martial
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repeat_region 3699. /note	3800 =="MSTA element fragment"	repeat_region	2350923800 /partial
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misc_feature 4957.	: !	misc_feature	complement (2554526171)
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	e="match: STS G15323" 5842	misc_feature	2619626539 /note="match: 5' RST H87640 clo
	e="L1 element fragment"	4	H87641 matching this cosmid"
repeat_region 5980. /note	6292 =="MLT2C2 element fragment"	misc_reature	complement(258282/189) /note="match: 3' EST H87629 clo
repeat_region 5980.	/onto. #4 mon olomont frammont	misc_feature	complement (2683327186)
repeat_region 6399.	eer mark arement tragment.		H87640 matching this cosmid"
/note: repeat region 7148.	/note="L1 element fragment" 71487437	repeat_region	2721927266 /note="24 copies of 2 mer 96 %
	partial noneat matches 308 1 of consensus"	repeat_region	27430, .27721 /partial
repeat_region 74607	. 7754 	, i	/porte="Alu repeat: matches 308.
	note="Alu repeat: matches 3081 of consensus"		/note="match: multiple ESTs"
repeat_region 94969 /partial		repeat_region	3004230333 /partial
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repeat_region 13166	308 OF C	noinear region	/note="Alu repeat: matches 1
repeat_region 14160	ישרכיובס די יסס סד	1011	/notes 15 copies of 2 mer 100 %
	e="Li element tragment" 616792	repeat_region	3313833433 /note="Alu repeat: matches 1
	/note="Alu repeat: matches 1308 of consensus" 1722017477	repeat_region	3355733894 /note="MLT1D element fragment"
	and	repeat_region	3391433989 /noter:WirlE element fragment"
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540 clone 252548; Paired with EST nid"
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nid"
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26176 CTCACTCTTCACCCATAATGTAGTAGACTACCTCCATTGTGTTGCTGTGCTGTCACCAGCACCC 26235
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                                                                                                                                                                                                                                                                                                                    /note="Alu repeat: matches 1. .62 of consensus"
7831 c 7983 g 11543 t
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Direct Submission

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 7030, USA
On Jul 14, 2002 this sequence version replaced gi:19718450.

Center: Baylor College of Medicine
Center: Condes BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Center project name: GTLM
Center clone name: GTLM
Center clone name: GTLM
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NOTE: This is a "working draft" sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                    Sequencing vector: Plaamid;
Sequencing vector: Plaamid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 1014166 bases at least Q30
Consensus quality: 111489 bases at least Q30
Consensus quality: 119214 bases at least Q30
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Mouse DNA sequence from clone RP23-182N4 on chromosome X, complete
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humquery@sanger.ac.uk Clone requests: clonerequeste@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:21213424.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115091 ACANTATTGAGAAAAACTTCAGCCGAGTTGGCACTCTGGTGGTACTGATTTCGGTCACCA 115032
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                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-182N4 is from the RPCI-23 Mouse PAC Library—constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
Location/Qualifiers
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0; Mismatches 90; Indels
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/db_xref="taxon:10090"
/chromosome="X"
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Matches 671; Conservative
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                                                                                                                                                                                                          121 AAGAAAGCACAGGAGGAGTTTCATCTTCGAAAGAAGAAATAGTCCTTGGCCAGAGACTCC 180
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                                                                                                         TATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGATCAAGTACGATG
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L Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science, Submission

L Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Pax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of Ecnomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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KRYKNWSUODAFLGSYPOLILOMYSIETIREWENDRALLMFSELLSYYGAIRCNYLA
IOSRODTTIKLPLIEFCVVWWRFLEVISRVYTALFIASIKUKSLEVILIYFVSI
LAPWIEFWKSGAHLPGNKENNSNWVGTVLMLFLITLLYAAINFSCWSAVKLOLSDDKI
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CGEVAFGLYMFEIYRKANDTFWMSFTISFIIVGAILDQIILMFFNKDLRRNKAALLFW
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MLLFYQYLYPWQSGKVLPGRTENQPEAPYYYVNIEKTEKNKNKQLRNYCNSCNRVGYF
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114731 TAGACTACCTCCATTGTATCTGCTGCCGCAGACCCCGTCCGGAAAGGTTGAGAACTCAG 114672
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                              TAGACTACCTCCATTGTGTCTGCTGTCACCAGCACCCTCGGACCAGGGTTGAGAACTCAG
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Pred. No. 8.8e-119;
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/db_xref="taxon:9606"
/clone="Tx705965"
/tissue_type="testis"
/clone_lib="Txr"
/note="cloning vector: pWE
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/db_xref="GI:21758667"
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Best Local Similarity
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'db_xref="G1:6502963"
'translation="MKFPASVIASVFLFVAETAAALYLSSTYRSAGDRWQVLTLLFS
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IATRVIVLVLPTSVLKIWVVAVILVNPFSFFLYPWIVFWCSGSPPPENIEKALSRVGT
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MYFFKTDIYMYVCAPLLILQLLIGYCTGILFMLVFYQFFHPCKKLFSSSVSESFRALL
RCACWSSLRRKSSEPVGRIDTDLKACTEQDVMPTTSKVIPEATDIWTAVDLCSA"
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Collec, E., Colin, Y., Carbonnet, F., Hattab, C., Bertrand, O., Cartron, J.P. and Kim, C.L.
Structure and expression of the mouse homologue of the XK gene Immunogenetics 50 (1-2), 16-21 (1999)
                                      1185
                                                               TIGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTG 1207
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          GCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGTTTTTAAGTTCT
                                 1126 TĊCTACACTACAGCTTTCAGTTTTAGAAATGTGATAATGATATTGGTATTTTAGGTTCT
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Mus musculus KX antigen (Xk) mRNA, complete cds.
AF155511 AF064772
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/dev_stage="8-12 weeks"
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'sex="male"
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Le Van Kim,C., Collec,E. and Colin,Y.
Direct Submission
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strain="BALB/c"
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chromosome="X"
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HSXKMTP 5096 bp mRNA linear PRI 19-MAY-1999
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Submitted (21-APR-1994) Meng F Ho, Human Genetics, Imperial Cancer Research Fund, Institute of Molecular Medicine John Radcliffe Hospital Headington, Oxford, OxON, Ox3 9DU, United Kingdom revised by [3]
3 (bases 1 to 5096)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 5096)

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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54.7%; Pred. No. 3e-72;
cive 0; Mismatches 508; Indels 12;
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Avalon Pharmaceuticals (US)
Location/Qualifiers
1. .5096
/organism="Homo sapiens"
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AX332514
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Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
Novel nucleic acids and polypeptides
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                     461 Gecanachartaceccheceartachececeacericatichaectrirerie
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                                                                                                                                                                                                      GAAGTCCTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTG
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                                                       514 CGGACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAGATCCAAGCCTTCCTG
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TIVLCFLTLLYTGINFCWSAVOLKIDSPDLISKSHWWYQLLYYWRRFIERALLLLL
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db_xref="GI:4883433"
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Direct Submission
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Submitted (121-0CT-1997) Meng F Ho, Human Genetics, Imperial Ca
Research Fund, Institute of Molecular Medicine John Radcliffe
Hospital Headingron, Oxford, OXON, OX3 9DU, United Kingdom
On May 20, 1999 this sequence version replaced gi:2570027.
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  Patent: WO 0222660-A 106 21-MAR-2002;
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                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
304. .1536
                                                        Location/Qualifiers
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Submitted (18-JUL-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 11368)
Cantu, L.A., McDermid, H. and Roe, B.A.
Homo sapiens Chromosome 22 PAC Clone p15j16 In CES Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-OCT-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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                                                TTCTGCTGGTCTGCTGTACAGCTGAAATTGACAGCCCTGACCTCATCAGCAAGTCCCAT 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGCAGCICATIATIGCITATCIGATTICCATIGGCTICATGCICCTTTTCTTCCAGTAC 1251
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On Feb 28, 2000 this sequence version replaced gi:6056215.
Because these overlapping clones came from different libraries
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Homo sapiens chromosome 22q11 clone p15j16, complete sequence
CGGGTCGGCACTCTGGTCGTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCAGAGAGATCTCGTCGACAAAGGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                    AATTGGTACCAGCTACTGGTGTATTACATGATTAGATTCATCGAGAATGCCATCCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCC
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Cantu, L.A., McDermid, H. and Roe, B.A.
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Cantu, L.A., McDermid, H. and Roe, B.A.
Direct Submission
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Cantu, L.A., McDermid, H. and Roe, B.A.
Direct Submission
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Homo sapiens Chromosome 22q11 PAC Clone p8708 in CES region,
complete sequence.
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                        nuclectide polymorphisms in the overlapping regions below. AC005301(p15j16) 77414 113688 (0) overlaps AC007064(p8708) 1 36275
there are numerous instances of insertions, deletions, and single
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 101469 ATACTGGCCATCCAGATCAGCAATGATGATACCATCAACCATAAGCTACCGCCGATAGAATTC 101410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101229 AATAATICCAATATGGTGGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCT 101170
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                             Length 113688;
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Pred. No. 3.1e-68;
0; Mismatches 220; Indels
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/organism="Homo sapiens"

/db_xref="raxon:9606"

/chromosome="22q11"

/clone="p15j16"

a 22385 c 21889 g 32256
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On Feb 29, 2000 this sequence version replaced gi:6249691.
Because these overlapping clones came from different libraries
there are numerous instances of insertions, deletions, and single
nucleotide polymorphisms in the overlapping regions below.
AC05301(pl516) 77414 113688 '(0) overlapp AC007064(p8708) 1 36275
(88548) AC007064 (p8708) 62616 124823 (0) overlaps AC006548(p20k14)
                                                                                                                                                                                                                                                                                  Submitted (11-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                               Ray, L.A., Loh, P., QI, S., Sloan, D., McDermid, H. and Roe, B.A. Direct Submission Submitted (26-OCT-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-OCT-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ray, L.A., Loh.P., Qi.S., Sloan, D., McDermid, H. and Roe, B.A.
Ray, L.A., Loh.P., Qi.S., Sloan, D., McDermid, H. and Roe, B.A.
Submission
Submitted (25-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-NOV-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-PEB-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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(bases 1 to 124823)
Ray, L.A., Loh, P., Qi, S., Sloan, D., McDermid, H. and Roe, B.A. Homo sapiens Chromosome 22q11 PAC Clone p8708 In CES Region Unpublished
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Ray L.A. Loh.P., Qi,S., Sloan,D., McDermid,H. and Roe,B.A. Direct Submission
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Ray, L.A., Loh, P., Qi,S., Sloan, D., McDermid, H. and Roe, B.A.
Direct Submission
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Ray, L.A., Loh, P., Qi, S., Sloan, D., McDermid, H. and Roe, B.A.
Direct Submission
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Unpublished 2 (bases 1 to 168918) Worley, K.C.
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alionoka, S.L., Amaratunge, H.C., Arg. J.R., Ayele, M., Banka, T., Barbaria, J., Banka, J., Banka, T., Barbaria, J., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elajo, C., Escotto, M., Falls, T., Ferragulo, D., Elagy, M., Forck, J., Foster, P., Frantz, P., Gabisi, A., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                               24116 ATAGCATTGCTGATGACATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAAT 24057
                                                                                                                                                                                                                                                                                    23936 TTCATTGCATCTCTGAAACTGAAGAGCCTACCCGTTTTGTTAATCATATTTTTGTATCA 23877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 CTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAAGATGCCCAATAACATTGAG 939
640 AGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGGCCACCCTTTGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          760 CTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTC
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volrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
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Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homari, F., Howard, S., Huber, J., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, B., Lu, K., Luna, R., May, J.,
Mabeshwari, M., Mapua, P., Martin, R., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkoo, S., Oguh, M., Okwuon, G.,
Oragunye, N., Nickerson, E., Nwokenko, S., Oguh, M., Okwuon, G.,
Peters, L., Pickens, R., Parims, E., Pu, L. L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Risson, I.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Tansey, J., Taylor, C., Taylor, P., Tamerisa, M., Thomas, S.,
Williams, G., Williamson, A., Wallington, C., Watlington, S.,
Wull, Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
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NOTE: This is a "working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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On Jul 14, 2002 this sequence version replaced gi:19718450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 168918)
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 104466 bases at least Q40
Consensus quality: 119214 bases at least Q20
Consensus quality: 119214 bases at least Q20
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1668: gap of unknown length
2687: contig of 1019 bp in length
2787: gap of unknown length
4137: contig of 1350 bp in length
4237: gap of unknown length
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contect: hgsc.help@bom.tmc.edu
Center project Information
Center project name: GTLM
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Mus musculus Strain C57BL6/J Chromosome X BAC, RP23-64A09, Complete Sequence, complete sequence.

AC091605.6 GI:22091329
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Montgomery,K.T., Grills,G., Li,L., Chiu,D., Decker,J., Fusina,M., Boltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E., High Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 122642 CAGATGTTTGGAGGCCATGATAAGTACCTTACACTGTGGAAGAAGAAGAGGGCCAGGAAGA 122701
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4: gap of unknown length
5: gap of unknown length
3: contig of 2048 bp in length
6: gap of unknown length
7: contig of 2987 bp in length
7: contig of 1711 bp in length
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7: contig of 2331 bp in length
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/gene="U43384 (Mm.200362) Mus musculus gp91phox (Cybb)"
/product="U43384 (Mm.200362) Mus musculus gp91phox (Cybb)"
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/rpt_family="RSINB1"
7096...7290
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complement(9054. .9070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db xref="taxon:10090"
chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64. .91
/rpt_family="AT_rich"
346. .401
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6853. .6895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="PB1D10"
6119. .6169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="RMBR4A"
6641. .6818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(CA)n"
complement(8098. .81
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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4825. .4971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="ID4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346. . . 401
/rpt_family="B1F"
complement(739. . 8
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6025. .6112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL6/J
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8042. .8092
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complement(8372.
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STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using Repeatmarker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCING READ COVERAGE: Attempts are made to complete double strandedsequence for all regions. All sequence is completed to a strandard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation aslow Coverage. Low coverage linkages are verified by PCR product size verification or verified and reverse reads from clones which span verification of forward and reverse reads from clones which span
Montgomery, K.T., Grills, G., Li, L., Chiu, D., Decker, J., Fusina, M., Goltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E., Perera, A., Shim, C., Thomas, E. and Kucherlapati, R..
Direct Submission
Submitted (09-MAY-2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
3 (bases 1 to 160200)
Montgomery, K.T., Grills, G., Li, L., Chiu, D., Decker, J., Fusina, M., Goltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                               Submitted (06-JUL-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                            Montgomery, K.T., Grills, G., Li, L., Chiu, D., Decker, J., Fusina, M., Goltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E., Perera, A., Shim, C., Thomas, E. and Kucherlapati, R. Direct Submission.
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Chemistry: Dye-terminator Big Dye; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Aug 2, 2002 this sequence version replaced gi:21700544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hpcgg.org/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r: Harvard Partners Genome Center
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9366. .9467 /rpt_family="PB1D7" complement(10128. .10335) /rpt_family="MER2B"

------ Distribution of Quality < 40 Bases:

Assembly program: Phrap version 0.990319 Contig length: 160200 Fraction of Phrap value < 40: 0.000736 Error Rate in Consed: 0.00 per 10,000 bases Number of N's in consensus: 0

/rpt_family="(TG)n" complement(9105..9282) /rpt_family="B3A" 9366..9467

/rpt_family="B3A" 9071. .9104

repeat_region repeat_region repeat_region repeat_region repeat_region

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AL672060 200698 bp DNA linear HTG 10-JUL-2002
Mus musculus chromosome X clone RP23-423L11, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 200698)
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Submitted (09-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
humquery@seanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 11, 2002 this sequence version replaced gi:21531232.
                                                                                                                                                                                             TIGCTTATCIGATTICCATIGGCTICATGCTCCTTTTCTTCCAGIACTTGCATCCATIGC 1264
                          1085 TGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATGATGGTCTTGGTTTTTTAAGT 1144
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AL672060.8 GI:21732098
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                          TCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATTA
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* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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1. .200698
/note="assembly_fragment:03870
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Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
------- Project Information
Center project name: bM423L11
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58266 a 4185<u>3</u> c 40587 g 59992
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/chromosome="X"
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DEFINITION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 143278 ATGAGTATGAGGTCAAAGTCAAACCCCTGGCTTATGTCTGTATCTTCCTCTGGAGAAGCT 143219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 143218 TTGAGATTGCCACCCGAGTCATCGTCCTGGTCCTCTTTACCTCTGTCCTGAAGATCTGGG 143159
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complement (1301. .13684)
/rpt_family="MTB"
14763. .14796
                                                                                                                                                                                      /rpt_family="(TGAA)n"
complement(16138. .16375)
/rpt_family="Lx6"
16882. .16568
/standard_name="BB222960"
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                                                                                                                                                                         Db 119410 AGGIGAGATITGACAGIGCICITICICITCICITCAGGCITCAICAIGACCITGICC 119469
                                                                                                                                                                                                                                                                                                                                                                                                                                     119590 TrGAGATTGCCACCCGAGTCATCGTCCTCGTCTTTACCTCTGTGCTGAGATCTGGG 119649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119770 CCATGGTGCTGGGTTCCTCACTTTACTCTATGCCGGCATCAACATGTTCTGCTGGTCAG 119829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 120010 TIGGGTACTGCACTGCATTCTCTTCATGCTTGTTCTATCAGTTTTTCCACCCTTGCA 120069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                Db 119470 TGCTGTCTATTGTCTATGGCGCCTTACGTTGCAACATCTTAGCCATCAAAATCAAGTATG 119529
                                                                                                                                                                                                                                                                                                                                                     ATGAGTATGAGGTCAAAGTCAAACCCCTGGCTTATGTCTGTATCTTCCTCTGGAGAAGCT 119589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 119650 rggrégcagrcaracrcgrcaactrcrrcagcrrcrrararcccreaarcgrricr 119709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119830 crerrcaderidaaaaredacaarecedadericardaddadrecedadadregraedee 119889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119890 TGCTCATTTACTACATGACGAGATTCATCGAGAACTCCGTCCTCCTGCTCTGTGGTATT 119949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119950 TTTTTAAAACTGACATATACATGTATGTGTGCGCCCTCTGTTGATCTTGCAGCTGCTTA 120009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   965 TGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTGCTGGTCAG 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTGCAGTTGAGGTTGGCAGACAGAGTCTCGTCGACAAAGGGCAGAACTGGGGACATA 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTGGAGTGAAAGTGTTACTGAATTACTGTCGTTGCTTGGTTGCCTTGCAGCTCATTA 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1205 TIGCTTATCTGATTCCATTGGCTTCATGCTCCTTTTCTTCCAGTACTTGCATTCCATTGC 1264
                                                                                                                                                                                                                     TGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGATCAAGTACG 724
                                                                                                                                                                                                                                                                                                            725 ATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACAT 784
                                                                                                                                                                                                                                                                                                                                                                                                 TGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGG 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            905 GGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTCGGCACTC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        845 CTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCCTGGATTAAGTTCT 904
                                                                                           Gaps
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Homo sapiens BAC clone RP11-506M9 from Y, complete sequence.
AC016752
                                                                                                                                605 ATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTAATGGTATTTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGTTTTTAAGT
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                                             Length 200698;
                                         15.7%; Score 218; DB 2; Length 20 llarity 57.5%; Pred. No. 6.7e-51; Conservative 0; Mismatches 290; Indels
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Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 166436)
Sulston, J.E. and Waterston, R.
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                                      Query Match
Best Local Similarity
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9847074
                                                                                  Matches 392;
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AUTHORS
TITLE
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Direct Submission
Submitted (25-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
7 (bases 1 to 166436)
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                                                                                                                                                                                                                   Direct Submission
Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
WO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (24.APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The position of this clone was established as part of a collaboration between the Human Chromosome Y Mapping Project (Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen, and David C. Page at the Whitehead Institute for Biomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (30-5EP-2000) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63
On Apr 23, 2000 this sequence version replaced gi:6524293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
Nguyen,C., Maupin,R., Hawkins,M. and Smith,R.
The sequence of Homo sapiens BAC clone RP11-506M9
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
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                                                                                                                                      3 (bases 1 to 166436)
Waterston, R.H.
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Waterston, R.H.
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Waterston, R.H.
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6 (bases 1 to 166436)
Waterston, R.H.
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Db 114404 AGCATTGCTGATGACATGTTCCTTCTTACCACTTGTATGCGGCCATTCACTGCAATAC 114345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 114106 TAATTCCAGCATGGTGGGTAC-ATACGGATGCTTAACTATATCATGCTACTATATGCTGC 114048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 114047 TATCAACTTCTCTGGCTGGTCAGCACTGAAACTGCAGCTCTCAAATGAGGAAGTAATTGA 113988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    942 AAACTTCAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGG 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 AGTIGIGCIAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATAT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 114284 CTG--TCATGATACGGTGTTCCTTGGTGATTATCTCACGTGTAGTGACTCTGGAATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702 GTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             762 CTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 166436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.6%; Score 217.2; DB 9; Length Best Local Similarity 62.3%; Pred. No. 1.1e-50; Matches 391; Conservative 0; Mismatches 233; Indels
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7rpt_family="Retroviral"

7rpt_family="Retroviral"

7rpt_family="Retroviral"

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35802. 35832
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                  The clone sequenced to the left is RP11-221K4. Actual start of this clone is at base position 1 of RP11-506M9; actual end is at base position 166436 of RP11-506M9.

Location/Qualifiers
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19815. 20107

/rpt family="Retroviral"

20410. 20861

/rpt family="Retroviral"

/rpt family="Retroviral"

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28006. .28520
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28828. .28905

    1. .166436
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/db_xref="taxon:9606"
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NEIGHBORING SEQUENCE INFORMATION:
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12836. .13209
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14667. .14689
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16692. .16712
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/rpt_family="AT_rich"
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/clone_lib="RPCI-11"
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17814. 18112
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19421. 19650
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9962. .10035
/rpt_family="L2"
10596. .10684
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7590. .17667
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28828. .28905
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29157. .29395
/rpt_family="Alu"
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/rpt_family="Alu"
3618. 3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alu"
4512 . 5804
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5804 . . 7682
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8188 . . 8294
                                                                                                                                                                                                                195. 923

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924. 1077

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1879. 1918
                                                                                                                                                                                                                                                                                                                            1879. . 1918
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1905. .3257
/rpt_family="L1"
3260. .3393
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9689. .19813
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29396. .29438
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswall Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-79J10; the clone sequenced to the left is RP11-79J10; the clone sequenced to the right is RP11-245K4, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-100J21; actual end is at base position 66964 of RP11-345K4.
                                                                            MAPPING INFORMATION:
The postition of this clone was established as part of a collaboration between the Human Chromosome Y Mapping Project (Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen, and David C. Page at the Whitchead Institute for Biomedical Research, Cambridge MA) and the Washington University Genome Sequencing Ceneer, St. Louis MO.
       more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .161879
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11"
1. .1185
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/rpt_family="ERVL"
3867, .6977
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/rpt_family="ERVL"
6986. .7295
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/rpt_family="ERVL"
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/rpt_family="ERV1"
16045. 16136
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7297. .7625
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Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 51109, USA
4 (bases 1 to 161879)
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5 (bases 1 to 161879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
Db 113987 CAAGAGACTGAGGTGGGC-CATAGAATCCTACACTACAGCTTCTAGTTTTTAGAAAATGT 113929
                                                                                              Db 113928 GATAATAATATTGATATTTATGTTCGTTGGAGGGAAATTTCACTGAAGTCTTGTGACTCT 113869
                                                                                                                                                                               Db 113868 ATTAATTGCCATGTAGTTCATCATAACCTAATTAGCCATTGGCTTTATGCTCTTT 113809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 'Chases 1 to 161879) Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                 AC017005
Homo sapiens BAC clone RP11-100/21 from Y, complete sequence.
AC017005
                                                 GATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTC
                                                                                                                                                CTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WGSSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-MAY-2001) Department of Genetics, Washington
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On Mar 23, 2001 this sequence version replaced gi:9211335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Armstrong, J., Stoneking, T., Hawkins, M. and Bernard, K. The sequence of Homo sapiens BAC clone RP11-100J21 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
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| Type | Family | ERV1 |
| 1788 | 17253 |
| 1746 | Family | ERV1 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160550 GTTGGCACCATGGCTGGAGTTTTGGAAAAGTGGAGCTCATCTTCATAACAACAACAAAAA 160609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OY 1182 CTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCTTTT 1241

Db 160848 ATTAATTGCCATGTAGTTCATCATAACCTAACTAATTAGCCATTGGCTTTATGCTCTCTT 160907
                                                                                                                                          Db 160312 AGCATTGCTGATGACATGTTCCTTACCACTTGTGTATGCGGCCATTCACTGCAATAC 160371
                                                                                                                                                                                                                                                      Db 160372 ACTGGCCATCCATACCAGCAACGACTTTCCTGACATTAAGCTACAAGCGATAAAATTCAT 160431
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                                                                                       AGTIGIGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCCACCCTTTGCAATAT 701
                                 Gaps
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                                                                                                                                                                                                   GTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCCTTGGGCCACTAGAAGTCCT
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                                                                                                                                                                                                                                                                                                                     CTGCATCACCATCTGGGGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTT
Best Local Similarity 62.1%; Pred. No. 3.2e-50;
Matches 390; Conservative 0; Mismatches 234; Indels
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Search completed: March 30, 2003, 05:28:41 Job time : 3999.31 secs

Length 161879; DB 9; 15.5%; Score 215.6;